

**AMENDMENTS TO THE CLAIMS**

The following listing of claims replaces all prior versions of claims in the application.

1. (Original): A protein consisting of an amino acid sequence represented by SEQ ID NO:1, or a salt thereof.

2. (Original): A protein consisting of an amino acid sequence represented by any one of SEQ ID NOS:3, 5, and 7, or a salt thereof.

3. (Original): A protein having an amino acid sequence derived from an amino acid sequence represented by SEQ ID NO:5 by deletion of 0 to 10 amino acid residues from the N-terminal and deletion of 0 to 5 amino acid residues from the C-terminal and having 92 to 106 amino acid residues, or a salt thereof.

4. (Currently amended): A protein consisting of an amino acid sequence derived from an amino acid sequence of a ~~protein~~ protein according to any one of claims 1, 2, [[and]] or 3 and having deletion, substitution or addition of one to several amino acids and having a function substantially identical with that of the protein according to claim 1, 2 or 3, or a salt thereof.

5. (Currently amended): A polynucleotide comprising a polynucleotide encoding an amino acid sequence of any one of proteins according to ~~claims 1 to 4~~ any one of claims 1, 2 or 3.

6. (Original): The polynucleotide according to claim 5, containing a nucleotide sequence represented by any one of SEQ ID NOS: 2, 4, 6, and 8.

7. (Currently amended): A recombinant vector containing a polynucleotide according to claim 5 [[or 6]].

8 (Currently amended) : A transformant which is transformed with a polynucleotide according to claim 5 [[or 6]].

9. (Currently amended) : An antibody against a protein according to any one of claims 1 [[to 4]] , 2 or 3.

10. (Currently amended): A method for producing a protein consisting of an amino acid sequence represented by SEQ ID NO:1 or a salt thereof ~~according to any one of claims 1 to 4~~, comprising the steps of culturing the transformant of claim 8 and producing the protein.

11. (Currently amended) : A method for producing a protein or a salt thereof according to any one of claims 1 [[to 4]] , 2 or 3, characterized by using a cell-free protein synthesis system.

12. (Currently amended): A method for screening a substance interacting with a protein or a salt thereof according to any one of claims 1 [[to 4]] , 2 or 3, and/or a naturally existing protein or a salt thereof containing an amino acid sequence of a protein according to any one of claims 1 [[to 4]] , 2 or 3, comprising the steps of bringing a candidate substance into contact with the protein of any one of claims 1 [[to 4]] , 2 or 3; and confirming whether the candidate substance interacts with the protein.

13. (Currently amended): A method for assaying a protein consisting of an amino acid sequence represented by SEQ ID NO:1 or a salt thereof ~~according to any one of claims 1 to 4~~ using an antibody of claim 9.

14. (Currently amended): A method for screening a substance interacting with a protein consisting of an amino acid sequence represented by SEQ ID NO:1 or a salt thereof according to any one of claims 1 to 4 using an assay method of claim 13.

15. (Currently amended): A method for specifying a gene associated with a protein according to any one of claims 1 [[to 4]] , 2 or 3, comprising the steps of expressing the protein according to any one of claims 1 [[to 4]] , 2 or 3, in a cell; and examining an expression status of the gene in the cell.

16. (Currently amended): A method for screening a substance interacting with a protein or a salt thereof according to any one of claims 1 [[to 4]] , 2 or 3, and/or a naturally existing protein or a salt thereof containing an amino acid sequence of a protein according to any one of claims 1 [[to 4]] , 2 or 3, comprising the steps of determining an active site of the protein using information concerning three-dimensional structure of the protein according to any one of claims 1 [[to 4]] , 2 or 3; and specifying a compound interacting with the active site on a computer.

17. (Original): The screening method according to claim 16, wherein the information concerning three-dimensional structure of the protein is three-dimensional structure information of a protein consisting of amino acid residues from amino acid 8 to amino acid 98 among three-dimensional structure information described in any of three-dimensional structure coordinate tables 1 to 20.

18. (Original): The screening method according to claim 17, wherein, among three-dimensional structure information described in three-dimensional structure coordinate table 1, a part of information corresponding to amino acid residues (Val26, Lys27, Glu47, Arg67, Lys83 and Ser86) is used.

19. (Currently amended): A method for screening a substance interacting with a protein consisting of an amino acid sequence represented by SEQ ID NO:1 or a salt thereof according to any one of claims 1 to 4 and/or a naturally existing protein or a salt thereof containing an amino acid sequence of a protein consisting of an amino acid sequence represented by SEQ ID NO:1 according to any one of claims 1 to 4, wherein a compound interacting with a specified active site is prepared as a candidate compound by a screening method according to any one of claims 16 to 18 claim 16, the method comprising the steps of bringing the candidate substance into contact with a protein consisting of an amino acid sequence represented by SEQ ID NO:1 according to any one of claims 1 to 4; and confirming whether the candidate substance has interaction with the protein.

20. (Currently amended): A method for presuming a three-dimensional structure of a protein with an unknown structure, wherein homology modeling is conducted on the protein with an unknown structure comprising an amino acid sequence having 30% or more homology with an amino acid sequence of a protein according to any one of claims 1 [[to 4]] , 2 or 3, by using information concerning three-dimensional structure information of a protein having amino acid residues from amino acid 8 to amino acid 98 among three-dimensional structures of a protein described in any of three-dimensional structure coordinate tables 1 to 20.